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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/068,804*

1641 #12

DATE: 01/28/99
TIME: 12:16:42

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APR 2 0 2000

TECH CENTER 1600/2900

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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```
 1                               SEQUENCE LISTING
 2
 3    (1)    General Information
 4
 5           (i) APPLICANT:  Miller, Samuel I.
 6
 7           (ii) TITLE OF THE INVENTION: SALMONELLA SECRETED PROTEINS
 8                    AND USES THEREOF
 9
10           (iii) NUMBER OF SEQUENCES: 47
11
12           (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: Fish & Richardson, P.C.
14              (B) STREET: 225 Franklin Street
15              (C) CITY: Boston
16              (D) STATE: MA
17              (E) COUNTRY: US
18              (F) ZIP: 02110-2804
19
20           (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Diskette
22              (B) COMPUTER: IBM Compatible
23              (C) OPERATING SYSTEM: Windows95
24              (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26           (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER:  09/068,804
28              (B) FILING DATE:  14-MAY-1998
29
30           (vii) PRIOR APPLICATION DATA:
31              (A) APPLICATION NUMBER: PCT/US96/18504
32              (B) FILING DATE: 14-NOV-1996
33
34              (A) APPLICATION NUMBER: 60/006,733
35              (B) FILING DATE: 14-NOV-1995
36
37           (viii) ATTORNEY/AGENT INFORMATION:
38              (A) NAME: Fraser, Janis K.
39              (B) REGISTRATION NUMBER: 34,819
40              (C) REFERENCE/DOCKET NUMBER: 00786/292002
41
42           (ix) TELECOMMUNICATION INFORMATION:
43              (A) TELEPHONE: 617-542-5070
44              (B) TELEFAX: 617-542-8906
45
46              (2) INFORMATION FOR SEQ ID NO:1:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/068,804*

DATE: 01/28/99
TIME: 12:16:43

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47
48          (i) SEQUENCE CHARACTERISTICS:
49             (A) LENGTH: 870 base pairs
50             (B) TYPE: nucleic acid
51             (C) STRANDEDNESS: double
52             (D) TOPOLOGY: linear
53
54          (ii) MOLECULE TYPE: Genomic DNA
55
56          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58   CGCAAAGCCG AGGAAACGAA CCGCATTATG GGATGTATCG GGAAAGTCCT CGGCGCGCTG      60
59   CTAACCATTG TCAGCGTTGT GGCCGCTGTT TTTACCGGTG GGGCGAGTCT GGCGCTGGCT     120
60   GCGGTGGGAC TTGCGGTAAT GGTGGCCGAT GAAATTGTGA AGGCGGCGAC GGGAGTGTCG     180
61   TTTATTCAGC AGGCGCTAAA CCCGATTATG GAGCATGTGC TGAAGCCGTT AATGGAGCTG     240
62   ATTGGCAAGG CGATTACCAA AGCGCTGGAA GGATTAGGCG TCGATAAGAA AACGGCAGAG     300
63   ATGGCCGGCA GCATTGTTGG TGCGATTGTC GCCGCTATTG CCATGGTGGC GGTCATTGTG     360
64   GTGGTCGCAG TTGTCGGGAA AGGCGCGGCG GCGAAACTGG GTAACGCGCT GAGCAAAATG     420
65   ATGGGCGAAA CGATTAAGAA GTTGGTGCCT AACGTGCTGA AACAGTTGGC GCAAAACGGC     480
66   AGCAAACTCT TTACCCAGGG GATGCAACGT ATTACTAGCG GTCTGGGTAA TGTGGGTAGC     540
67   AAGATGGGCC TGCAAACGAA TGCCTTAAGT AAAGAGCTGG TAGGTAATAC CCTAAATAAA     600
68   GTGGCGTTGG GCATGGAAGT CACGAATACC GCAGCCCAGT CAGCCGGTGG TGTTGCCGAG     660
69   GGCGTATTTA TTAAAAATGC CAGCGAGGCG CTTGCTGATT TTATGCTCGC CCGTTTTGCC     720
70   ATGGATCAGA TTCAGCAGTG GCTTAAACAA TCCGTAGAAA TATTTGGTGA AAACCAGAAG     780
71   GTAACGGCGG AACTGCAAAA AGCCATGTCT TCTGCGGTAC AGCAAAATGC GGATGCTTCG     840
72   CGTTTTATTC TGCGCCAGAG TCGCGCATAA                                       870
73
74          (2) INFORMATION FOR SEQ ID NO:2:
75
76          (i) SEQUENCE CHARACTERISTICS:
77             (A) LENGTH: 1230 base pairs
78             (B) TYPE: nucleic acid
79             (C) STRANDEDNESS: double
80             (D) TOPOLOGY: linear
81
82          (ii) MOLECULE TYPE: Genomic DNA
83
84          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
85
86   ATGTTAATTA GTAATGTGGG AATAAATCCC GCCGCTTATT TAAATAATCA TTCTGTTGAG      60
87   AATAGTTCAC AGACAGCTTC GCAATCCGTT AGCGCTAAAG ATATTCTGAA TAGTATTGGT     120
88   ATTAGCAGCA GTAAAGTCAG TGACCTGGGG TTGAGTCCTA CACTGAGCGC GCCTGCGCCA     180
89   GGGGTATTAA CGCAAACCCC CGGAACGATC ACGTCCTTTT TAAAAGCCAG TATTCAAAAT     240
90   ACCGACATGA ATCAGGATTT GAATGCTCTG GCAAATAATG TCACGACTAA AGCGAATGAG     300
91   GTTGTGCAAA CCCAGTTACG CGAGCAGCAG GCAGAAGTCG GAAAGTTTTT TGATATTAGC     360
92   GGAATGTCTT CCAGTGCCGT TGCGCTGTTG GCTGCCGCGA ATACGTTAAT GCTGACGTTG     420
93   AACCAGGCTG ATAGCAAACT GTCTGGTAAG TTGTCATTAG TCAGTTTTGA TGCAGCTAAA     480
94   ACGACGGCAA GCTCCATGAT GCGCGAAGGG ATGAATGCGT TGTCCGGTAG TATTTCCCAG     540
95   AGCGCGCTTC AGTTGGGGAT CACTGGCGTG GGCGCCAAAC TGGAATATAA GGGGCTGCAG     600
96   AATGAAAGAG GCGCGCTTAA ACATAATGCC GCGAAGATCG ATAAACTGAC CACTGAAAGC     660
97   CACAGTATTA AAAACGTGCT GAACGGGCAG AATAGCGTCA AACTCGGTGC TGAAGGCGTC     720
98   GATTCTCTGA AATCGTTAAA TATGAAGAAA ACCGGTACCG ATGCGACGAA AAATCTTAAT     780
99   GATGCGACGC TTAAATCTAA TGCCGGAACC AGCGCCACGG AAAGTCTGGG TATTAAAGAC     840
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100   AGTAATAAAC AAATCTCCCC TGAACATCAG GCTATTCTGT CGAAACGTCT TGAGTCTGTC      900
101   GAATCCGATA TTCGTCTTGA GCAGAATACC ATGGATATGA CCCGAATCGA TGCGCGCAAG      960
102   ATGCAGATGA CGGGCGATCT GATTATGAAG AACTCGGTCA CGGTCGGTGG TATTGCAGGG     1020
103   GCGTCCGGGC AGTACGCCGC TACTCAGGAA CGTTCCGAGC AGCAAATTAG CCAGGTGAAT     1080
104   AACCGGGTTG CCAGCACCGC ATCGGACGAA GCCCGTGAAA GTTCACGTAA ATCGACCAGC     1140
105   CTGATTCAGG AAATGCTGAA AACAATGGAG AGCATTAACC AGTCGAAAGC ATCCGCACTC     1200
106   GCTGCTATCG CAGGCAATAT TCGCGCTTAA                                      1230
107
108               (2) INFORMATION FOR SEQ ID NO:3:
109
110         (i) SEQUENCE CHARACTERISTICS:
111            (A) LENGTH: 1032 base pairs
112            (B) TYPE: nucleic acid
113            (C) STRANDEDNESS: double
114            (D) TOPOLOGY: linear
115
116         (ii) MOLECULE TYPE: Genomic DNA
117
118         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
119
120   ATGCTTAATA TTCAAAATTA TTCCGCTTCT CCTCATCCGG GGATCGTTGC CGAACGGCCG       60
121   CAGACTCCCT CGGCGAGCGA GCACGTCGAG ACTGCCGTGG TACCGTCTAC CACAGAACAT      120
122   CGCGGTACAG ATATCATTTC ATTATCGCAG GCGGCTACTA AAATCCACCA GGCACAGCAG      180
123   ACGCTGCAGT CAACGCCACC GATCTCTGAA GAGAATAATG ACGAGCGCAC GCTGGCGCGC      240
124   CAGCAGTTGA CCAGCAGCCT GAATGCGCTG GCGAAGTCCG GCGTGTCATT ATCCGCAGAA      300
125   CAAAATGAGA ACCTGCGGAG CGCGTTTTCT GCGCCGACGT CGGCCTTATT TAGCGCTTCG      360
126   CCTATGGCGC AGCCGAGAAC AACCATTTCT GATGCTGAGA TTTGGGATAT GGTTTCCCAA      420
127   AATATATCGG CGATAGGTGA CAGCTATCTG GGCGTTTATG AAAACGTTGT CGCAGTCTAT      480
128   ACCGATTTTT ATCAGGCCTT CAGTGATATT CTTTCCAAAA TGGGAGGCTG GTTATTACCA      540
129   GGTAAGGACG GTAATACCGT TAAGCTAGAT GTTACCTCAC TCAAAAATGA TTTAAACAGT      600
130   TTAGTCAATA AATATAATCA AATAAACAGT AATACCGTTT TATTTCCAGC GCAGTCAGGC      660
131   AGCGGCGTTA AAGTAGCCAC TGAAGCGGAA GCGAGACAGT GGCTCAGTGA ATTGAATTTA      720
132   CCGAATAGCT GCCTGAAATC TTATGGATCC GGTTATGTCG TCACCGTTGA TCTGACGCCA      780
133   TTACAAAAAA TGGTTCAGGA TATTGATGGT TTAGGCGCGC CGGGAAAAGA CTCAAAACTC      840
134   GAAATGGATA ACGCCAAATA TCAAGCCTGG CAGTCGGGTT TTAAAGCGCA GGAAGAAAAT      900
135   ATGAAAACCA CATTACAGAC GCTGACGCAA AAATATAGCA ATGCCAATTC ATTGTACGAC      960
136   AACCTGGTAA AAGTGCTGAG CAGTACGATA AGTAGCAGCC TGGAAACCGC CAAAAGCTTC     1020
137   CTGCAAGGAT AA                                                         1032
138
139               (2) INFORMATION FOR SEQ ID NO:4:
140
141         (i) SEQUENCE CHARACTERISTICS:
142            (A) LENGTH: 194 base pairs
143            (B) TYPE: nucleic acid
144            (C) STRANDEDNESS: double
145            (D) TOPOLOGY: linear
146
147         (ii) MOLECULE TYPE: Genomic DNA
148
149         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
150
151   ATGGTTACAA GTGTAAGGAC TCAGCCCCCC GTCATAATGC CAGGTATGCA GACCGAGATC       60
152   AAAACGCAGG CCACGAATCT TGCGGCGAAT CTTTCCGCAG TCAGAGAAAG TGCCACAGCG      120
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153   ACGCTGTCAG GGGAAATTAA AGGCCCGCAA CTGGAAGATT TTCCCGCGCT GATCAAACAG   180
154   GCGAGTCTGG ATGC                                                     194
155
156           (2) INFORMATION FOR SEQ ID NO:5:
157
158           (i) SEQUENCE CHARACTERISTICS:
159             (A) LENGTH: 290 amino acids
160             (B) TYPE: amino acid
161             (D) TOPOLOGY: linear
162
163           (ii) MOLECULE TYPE: peptide
164
165           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
166
167   Arg Lys Ala Glu Glu Thr Asn Arg Ile Met Gly Cys Ile Gly Lys Val
168    1               5                  10                  15
169   Leu Gly Ala Leu Leu Thr Ile Val Ser Val Val Ala Ala Val Phe Thr
170             20                  25                  30
171   Gly Gly Ala Ser Leu Ala Leu Ala Ala Val Gly Leu Ala Val Met Val
172             35                  40                  45
173   Ala Asp Glu Ile Val Lys Ala Ala Thr Gly Val Ser Phe Ile Gln Gln
174        50                  55                  60
175   Ala Leu Asn Pro Ile Met Glu His Val Leu Lys Pro Leu Met Glu Leu
176    65                  70                  75                  80
177   Ile Gly Lys Ala Ile Thr Lys Ala Leu Glu Gly Leu Gly Val Asp Arg
178             85                  90                  95
179   Lys Arg Gln Arg Trp Pro Ala Ala Leu Leu Val Arg Leu Ser Pro Leu
180             100                 105                 110
181   Cys His Gly Asp Ala Val Ile Val Val Val Ala Val Val Gly Lys Gly
182             115                 120                 125
183   Ala Ala Ala Lys Leu Gly Asn Ala Leu Ser Lys Met Met Gly Glu Thr
184        130                 135                 140
185   Ile Lys Lys Leu Val Pro Asn Val Leu Lys Gln Leu Ala Gln Asn Gly
186    145                 150                 155                 160
187   Ser Lys Leu Phe Thr Gln Gly Met Gln Arg Ile Thr Ser Gly Leu Gly
188             165                 170                 175
189   Asn Val Gly Ser Lys Met Gly Leu Gln Thr Asn Ala Leu Ser Lys Glu
190             180                 185                 190
191   Leu Val Gly Asn Thr Leu Asn Lys Val Ala Leu Gly Met Glu Val Thr
192             195                 200                 205
193   Asn Thr Ala Ala Gln Ser Ala Gly Gly Val Ala Glu Gly Val Phe Ile
194        210                 215                 220
195   Lys Asn Ala Ser Glu Ala Leu Ala Asp Phe Met Leu Ala Arg Phe Ala
196   225                 230                 235                 240
197   Met Asp Gln Ile Gln Gln Trp Leu Lys Gln Ser Val Glu Ile Phe Gly
198             245                 250                 255
199   Glu Asn Gln Lys Val Thr Ala Glu Leu Gln Lys Ala Met Ser Ser Ala
200             260                 265                 270
201   Val Gln Gln Asn Ala Asp Ala Ser Arg Phe Ile Leu Arg Gln Ser Arg
202        275                 280                 285
203   Ala Glx
204        290
205
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206              (2) INFORMATION FOR SEQ ID NO:6:
207
208          (i) SEQUENCE CHARACTERISTICS:
209              (A) LENGTH: 410 amino acids
210              (B) TYPE: amino acid
211              (D) TOPOLOGY: linear
212
213          (ii) MOLECULE TYPE: peptide
214
215          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
216
217    Met Leu Ile Ser Asn Val Gly Ile Asn Pro Ala Ala Tyr Leu Asn Asn
218     1               5                  10                  15
219    His Ser Val Glu Asn Ser Ser Gln Thr Ala Ser Gln Ser Val Ser Ala
220                20                  25                  30
221    Lys Asp Ile Leu Asn Ser Ile Gly Ile Ser Ser Ser Lys Val Ser Asp
222                35                  40                  45
223    Leu Gly Leu Ser Pro Thr Leu Ser Ala Pro Ala Pro Gly Val Leu Thr
224         50                  55                  60
225    Gln Thr Pro Gly Thr Ile Thr Ser Phe Leu Lys Ala Ser Ile Gln Asn
226     65                  70                  75                  80
227    Thr Asp Met Asn Gln Asp Leu Asn Ala Leu Ala Asn Asn Val Thr Thr
228                85                  90                  95
229    Lys Ala Asn Glu Val Val Gln Thr Gln Leu Arg Glu Gln Gln Ala Glu
230                100                 105                 110
231    Val Gly Lys Phe Phe Asp Ile Ser Gly Met Ser Ser Ser Ala Val Ala
232                115                 120                 125
233    Leu Leu Ala Ala Ala Asn Thr Leu Met Leu Thr Leu Asn Gln Ala Asp
234         130                 135                 140
235    Ser Lys Leu Ser Gly Lys Leu Ser Leu Val Ser Phe Asp Ala Ala Lys
236     145                 150                 155                 160
237    Thr Thr Ala Ser Ser Met Met Arg Glu Gly Met Asn Ala Leu Ser Gly
238                165                 170                 175
239    Ser Ile Ser Gln Ser Ala Leu Gln Leu Gly Ile Thr Gly Val Gly Ala
240                180                 185                 190
241    Lys Leu Glu Tyr Lys Gly Leu Gln Asn Glu Arg Gly Ala Leu Lys His
242                195                 200                 205
243    Asn Ala Ala Lys Ile Asp Lys Leu Thr Thr Glu Ser His Ser Ile Lys
244         210                 215                 220
245    Asn Val Leu Asn Gly Gln Asn Ser Val Lys Leu Gly Ala Glu Gly Val
246     225                 230                 235                 240
247    Asp Ser Leu Lys Ser Leu Asn Met Lys Lys Thr Gly Thr Asp Ala Thr
248                245                 250                 255
249    Lys Asn Leu Asn Asp Ala Thr Leu Lys Ser Asn Ala Gly Thr Ser Ala
250                260                 265                 270
251    Thr Glu Ser Leu Gly Ile Lys Asp Ser Asn Lys Gln Ile Ser Pro Glu
252                275                 280                 285
253    His Gln Ala Ile Leu Ser Lys Arg Leu Glu Ser Val Glu Ser Asp Ile
254         290                 295                 300
255    Arg Leu Glu Gln Asn Thr Met Asp Met Thr Arg Ile Asp Ala Arg Lys
256     305                 310                 315                 320
257    Met Gln Met Thr Gly Asp Leu Ile Met Lys Asn Ser Val Thr Val Gly
258                325                 330                 335
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SEQUENCE VERIFICATION REPORT
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DATE: 01/28/99
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